Emerging functional roles of nuclear receptors in breast cancer

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Abstract

Nuclear receptors (NRs) have been targets of intensive drug development for decades due to their roles as key regulators of multiple developmental, physiological and disease processes. In breast cancer, expression of the estrogen and progesterone receptor remains clinically important in predicting prognosis and determining therapeutic strategies. More recently, there is growing evidence supporting the involvement of multiple nuclear receptors other than the estrogen and progesterone receptors, in the regulation of various processes important to the initiation and progression of breast cancer. We review new insights into the mechanisms of action of NRs made possible by recent advances in genomic technologies and focus on the emerging functional roles of NRs in breast cancer biology, including their involvement in circadian regulation, metabolic reprogramming and breast cancer migration and metastasis.

Introduction

Breast cancer is the most common cancer diagnosed in women worldwide (Ferlay et al. 2015). Over the past decades, substantial progress toward treatment of primary estrogen receptor-positive (ER+) breast cancer has been made with the development of endocrine therapies targeting the estrogen biosynthesis and signaling pathways. Despite the success of endocrine therapies, there remain subgroups of women for whom available treatment offers little help. These include patients with ER+ breast tumors who develop endocrine treatment resistance (Dixon 2014), patients with estrogen receptor-negative (ER−) breast cancers (Hudis & Gianni 2011) and cancers that recur in all age groups (EBCTCG 2005). Women in these subgroups currently face the challenge of living with advanced disease; therefore, there exists the need to develop rational treatments targeting these subgroups of breast cancer.

Nuclear receptors (NRs) are potential promising targets due to the importance of NRs as master regulators of nearly all physiological aspects of life and the availability of drugs targeting NRs that resulted from intensive drug development targeting NRs for a range of pathological conditions. The human NR superfamily consists of 48 highly evolutionarily conserved transcription factors with the ability to act as molecular sensors of physiological and environmental stimuli (Mangelsdorf et al. 1995). Development of technologies that allow genome-wide, unbiased profiling of genomic binding sites and gene expression has allowed deeper insights into the molecular mechanisms of NR actions. These studies highlight the complexity of gene regulatory networks governed by NRs, the extensive nature of NR crosstalk and the role of coregulators and the chromatin landscape of the cell as important modulators of NR cell type-specific and context-dependent function.

In the context of breast cancer, it is recognized that estrogen receptor (ESR1) and progesterone receptor (PGR) play critical roles in the development and progression of disease; therefore, the need to target these NRs with new therapies is essential. In this review, we focus on the emerging functional roles of NRs in breast cancer biology, including their involvement in circadian regulation, metabolic reprogramming and breast cancer migration and metastasis.

Key Words

- nuclear receptors
- breast cancer
- circadian clock
- metabolism
- migration and metastasis
of breast cancer, and moreover, their expression in a breast tumor remains the single most robust predictor of disease outcome. Consequently, measurement of ESR1 and PGR expression in breast cancers is a mainstay of clinical management programs and treatments targeting the estrogen signaling axis are standard of care for ER+ disease (Cordera & Jordan 2006). More recently, the androgen receptor (AR), which is frequently expressed in primary breast tumors (Park et al. 2010, Grogg et al. 2015), has emerged both as a marker of outcome and as a potential treatment target (Cordera & Jordan 2006, Barton et al. 2015). A number of other nuclear receptors, including the vitamin D3 receptor (VDR) (Krishnan et al. 2010, Mehta et al. 2013) and the glucocorticoid receptor (GR) (Vilasco et al. 2011, Abduljabbar et al. 2015b) have also been investigated for their anti-proliferative and anti-apoptotic effects in breast cancer. Members of the retinoid receptor subfamily have also received considerable attention, particularly the crosstalk between the retinoic acid receptor alpha (RARA) and estrogen signaling (Hua et al. 2009, Ross-Innes et al. 2010), and the anti-migratory effect of the retinoic acid receptor beta (RARB) in breast cancer (Yang et al. 2002, Flaminì et al. 2014). However, the functional roles of the majority of the remaining members of the human NR family in the normal breast and breast cancer have largely been unexplored. Recent studies are establishing that the involvement of NRs in breast cancer extends beyond their involvement in regulating proliferation and apoptosis and that NRs are important regulators of several aspects of breast cancer tumorigenesis and progression including regulation of the circadian clock, metabolism, migration and metastasis. In this review, we will discuss evidence for these emerging functional roles of NRs in breast cancer, as well as new insights into the molecular mechanisms of action of NRs made possible through advances in genomic technologies.

The nuclear receptor superfamily

The human nuclear receptor superfamily consists of 48 members. These transcription factors include the receptors for steroid hormones, thyroid hormones, lipophilic vitamins and cholesterol metabolites including retinoic acid and oxysterols (Mangelsdorf et al. 1995). Members of the NR superfamily are identified through their highly evolutionarily conserved structural organization (Evans & Mangelsdorf 2014), which consists of four major domains: The N-terminal A/B domain with activation function1 (AF1); the DNA-binding domain (DBD) consisting of two zinc finger motifs which confers response element specificity and the hinge region linking the DBD to the ligand-binding domain (LBD), which may or may not have an AF2 region that mediates coactivator interaction (Giguère et al. 1986, Kumar et al. 1987, Mangelsdorf et al. 1995) (Fig. 1A). Approximately half of the NRs are designated as orphans because endogenous physiological ligands for these NRs have not been found (Table 1). The 48 human NRs are organized into six evolutionary groups based on sequence alignment and phylogenetic tree construction (Auwerx et al. 1999, Germain et al. 2006). Organization of NRs into functional groupings is also feasible, based on profiling the anatomical expression of NRs. In the mouse, this revealed a hierarchical organization of NRs into integrated physiologic functional groups (Fig. 1B), which partially reflect the functional groupings observed in human, especially for NRs that are involved in circadian and metabolic pathways (reviewed here).

In the classical model of NR action, upon ligand activation, NRs regulate gene transcription by binding response elements within the regulatory regions of target genes as monomers, homodimers or heterodimers with another family member. For example, steroid hormone receptors generally bind as homodimers, whereas VDR, THR, RAR and RXR can form both homodimers and heterodimers. RXRs in particular can act as promiscuous heterodimerization partners for VDR, THR, RAR and orphan receptors. Dimerization is a general mechanism to increase binding affinity, specificity and diversity. Nuclear receptor response elements are derivatives of the canonical hexameric sequence RGGTCA. Modifications and duplications (organized as direct, inverted or everted repeats separated by a spacer with variable length) of this canonical hormone response element allow for selective recognition by different NR subclasses (Laudet & Gronemeyer 2002, Gronemeyer et al. 2004).

Ligand binding also allosterically controls the interaction of NRs with coregulators by influencing the conformation of the AF2 region. Coregulators are integral to the mechanisms by which NRs exert their functions and include both coactivators and corepressors. The majority of coregulators function as members of large complexes that affect NR transcriptional regulation of target genes through interactions with other transcription factors, the chromatin landscape as well as non-coding RNAs (Millard et al. 2013). Both the interaction with coregulators and the chromatin landscape of the cell have been shown to affect the cell type specificity of NRs.

NRs regulate the transcription of genes that control a wide variety of biological processes in normal physiology.
including embryonic development, reproduction, metabolism, homeostasis and cell proliferation. NRs are also known to play a role in various pathological processes including cancer, inflammation and metabolic disorders (McKenna & O’Malley 2010) and as such have been targets of intensive drug development for decades (Ottow & Weinmann 2008).

**NR expression in the normal breast and breast cancer**

Recent studies have begun to provide a global view of the functional roles and expression of the NR superfamily in primary normal breast (Muscat et al. 2013) and breast cancer tissues (Muscat et al. 2013, Lin et al. 2015). Muscat and coworkers found that the majority of NRs are expressed in the breast (41 of 48). Many NRs showed differential expression in breast cancer compared to the normal breast indicative of potential involvement in breast cancer biology (Muscat et al. 2013). In particular, breast cancer is associated with the overexpression of the NR4A subgroup as well as EAR2, and pan-repression of the majority of NRs relative to the normal breast. High expression of the NR4A subgroup in breast cancer was also observed by Lin and coworkers (Lin et al. 2015). In addition to ESR1, PGR and AR, expression levels of other NRs were shown to be associated with histological grade (THRB, NUR77, RORC, COUP-TF2 and LRH-1), to classify breast tissues (THRA, ESR1, NURR77, EAR2 and RARG) and to predict metastasis-free survival in tamoxifen-treated patients (THRB, COUP-TF2, MR and PPARG). Thirty-three of the 48 human NRs were also observed to be expressed in stromal cells and four of these (RORA, THRB, VDR and PPARG) were shown to have differential expression profiles in cancer-associated fibroblasts compared to normal breast adipose fibroblasts (Knower et al. 2013). Together, these studies highlight that multiple members of the NR family are likely to play important roles in breast cancer growth and development and to have discriminant and prognostic value in breast cancer.

**NR expression in breast cancer subtypes**

Breast cancer is a heterogeneous disease encompassing multiple subtypes with distinct molecular profiles, therapeutic response and clinical outcomes (Prat et al. 2015). Several NRs have been shown to either act co-operatively with ESR1 and/or have differential...
# Table 1  Human nuclear receptors.

<table>
<thead>
<tr>
<th>Name</th>
<th>Nomenclature</th>
<th>Symbol</th>
<th>Entrez ID</th>
<th>Ligands</th>
<th>Expression in BC vs normal</th>
<th>Association with ESR1 expression</th>
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<td></td>
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<td>Estrogen receptor</td>
<td>NR3A1</td>
<td>ESR1</td>
<td>2099</td>
<td>Estrogens</td>
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<td>NR3A2</td>
<td>ESR2</td>
<td>2100</td>
<td>Estradiols</td>
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<td>NR3C1</td>
<td>GR</td>
<td>2908</td>
<td>Cortisols, aldosterone</td>
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<td>MR</td>
<td>4306</td>
<td>Testosterone, dihydrotestosterone</td>
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<td><strong>Non-steroid hormone receptors</strong></td>
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<td>THRA</td>
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<td></td>
<td>NR1A2</td>
<td>THR8</td>
<td>7068</td>
<td>Thyroxine (T&lt;sub&gt;4&lt;/sub&gt;), triiodothyronine (T&lt;sub&gt;3&lt;/sub&gt;)</td>
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<td>Yes&lt;sup&gt;a,b&lt;/sup&gt;</td>
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<td>RARA</td>
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<td>RARB</td>
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<td>RORB</td>
<td>6096</td>
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<td>Decreased</td>
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<td>NR1F3</td>
<td>RORC</td>
<td>6097</td>
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<td>VDR</td>
<td>7421</td>
<td>Calcitriol (1,25-dihydroxy vitamin D&lt;sub&gt;3&lt;/sub&gt;)</td>
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<td></td>
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<td>Peroxisome proliferator-</td>
<td>NR1C1</td>
<td>PPARA</td>
<td>5465</td>
<td>Fatty acids</td>
<td>Decreased</td>
<td>Yes&lt;sup&gt;b&lt;/sup&gt;</td>
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<td>activated receptor</td>
<td>NR1C2</td>
<td>PPARD</td>
<td>5467</td>
<td>Fatty acids</td>
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<td>NR1C3</td>
<td>PPARG</td>
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<td>Fatty acids</td>
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<td>NR1D1</td>
<td>REV-ERBa</td>
<td>9572</td>
<td>Heme</td>
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<td>REV-ERBb</td>
<td>9975</td>
<td>Heme</td>
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<td>Liver X receptor-like</td>
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<td>LXRb</td>
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<td>NR1H3</td>
<td>LXRa</td>
<td>10062</td>
<td>Oxyesters</td>
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<td>PXR</td>
<td>8856</td>
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<td>NR1I3</td>
<td>CAR</td>
<td>9970</td>
<td>Androstanol, androstenol</td>
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<td>NR2B1</td>
<td>RXRA</td>
<td>6256</td>
<td>9-cis-retinoic acid</td>
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<td>NR2B2</td>
<td>RXRB</td>
<td>6257</td>
<td>9-cis-retinoic acid</td>
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<td>Steroidogenic factor-like</td>
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<td>SF-1</td>
<td>2516</td>
<td>Phospholipids</td>
<td>Not expressed</td>
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<td>Orphan nuclear receptors</td>
<td>NR5A2</td>
<td>LRH-1</td>
<td>2494</td>
<td>Phospholipids</td>
<td>Decreased</td>
<td>Yes&lt;sup&gt;b&lt;/sup&gt;</td>
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<td>DSS-AHC critical region on the X chromosome, gene 1</td>
<td>NR0B1</td>
<td>DAX-1</td>
<td>Not known</td>
<td>Not known</td>
<td>Not expressed</td>
<td>Yes</td>
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<td>Short heterodimeric partner</td>
<td>NR0B2</td>
<td>SHP</td>
<td>8431</td>
<td>CD437 retinoids</td>
<td>Not expressed</td>
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<td>Hepatocyte nuclear factor 4</td>
<td>NR2A1</td>
<td>HNF4a</td>
<td>3172</td>
<td>Fatty acids</td>
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<td>NR2A2</td>
<td>HNF4g</td>
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<td>TR2</td>
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<td>TR4</td>
<td>7182</td>
<td>All-trans retinoic acid</td>
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<td>Tailless-related receptor</td>
<td>NR2E1</td>
<td>TLX</td>
<td>7101</td>
<td>Not known</td>
<td>Decreased</td>
<td>Yes&lt;sup&gt;b&lt;/sup&gt;</td>
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<td>Photoreceptor cell-specific receptor</td>
<td>NR2E3</td>
<td>PNR</td>
<td>10002</td>
<td>Benzimidazoles</td>
<td>Decreased</td>
<td>Yes&lt;sup&gt;a,b&lt;/sup&gt;</td>
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<td>Chicken ovalbumin upstream promoter-transcription factor</td>
<td>NR2F1</td>
<td>COUP-TF1</td>
<td>7025</td>
<td>Not known</td>
<td>Decreased</td>
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<td></td>
<td>NR2F2</td>
<td>COUP-TF2</td>
<td>7026</td>
<td>Retinol/ATRA</td>
<td>Decreased</td>
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</tr>
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(Continued)
actions in ER+ vs ER− breast cancers. For instance, AR has different roles in ER+ vs ER− breast cancers. AR has been investigated extensively as a therapeutic target in ER− breast cancer. It was reported that in ER−/HER2+ breast tumors, AR stimulates oncogenic Wnt and HER2 signaling pathways thereby stimulating cancer cell growth (Ni et al. 2011). However, the role of androgen signaling in ER+ breast cancer is less clear. Expression of AR is associated with good prognosis in ER+ breast cancer (Hu et al. 2011, Hilborn et al. 2016), with anti-estrogenic and anti-proliferative effects in ER+ breast cancer being reported (Peters et al. 2009, D’Amato et al. 2015). The anti-proliferative effect of AR is partly attributed to its inhibitory effect on ESR1 signaling in ER+ breast cancer cells (Peters et al. 2009, Fioretti et al. 2014). However, AR has also been reported to contribute to therapy resistance in ER+ breast cancer cells overexpressing AR, with increase in AR-to-ESR1 ratio associated with worse outcome for tamoxifen-treated patients (Cochrane et al. 2014) and increased agonist activity of Tam in AR overexpressing cells. In this context, AR reportedly increased tamoxifen agonist activity via the activation of EGFR in ER+ breast cancer, and this was blocked by dual treatment with the anti-androgen enzalutamide and EGFR inhibitor gefitinib (Ciupek et al. 2015). In addition, AR appears to promote proliferation of molecular apocrine breast cancer; a subset of TNBC expressing AR, through activation of genes that are normally regulated by ESR1 in ER+ cancer (Robinson et al. 2011).

Similarly, the expression of GR has been shown to be differentially associated with survival in ER+ vs ER− breast cancers. In ER+ breast cancers, high GR expression is associated with better survival (Pan et al. 2011, Abduljabbar et al. 2015b), whereas in ER− breast cancers, high GR expression is correlated with poorer breast cancer-specific survival (Pan et al. 2011, Abduljabbar et al. 2015b).

Recent studies profiling the expression of NRs in ER+ and ER− cancers have also identified other NRs whose expression levels differ significantly between ER+ and ER− breast cancers (Table 1). In particular, AR, PGR, PNR, RARA and THRB were reported to be significantly associated with ESR1 expression (Muscat et al. 2013) and significantly associated with ESR1 expression (Lin et al. 2015). The expression of DAX-1, LRH-1, PPARA, RORB, RORC and TLX were also reported to be significantly associated with ESR1 expression in multiple microarray datasets (Lin et al. 2015).

### Mechanisms of NR action

Alterations in normal transcriptional programs are a fundamental feature of cancer pathogenesis and progression. Nuclear receptors are important regulators that directly couple small-molecule signaling with transcriptional regulation. An understanding of their mechanisms of action at the genomic and network level, and how these processes are altered in breast cancer, is of
fundamental importance to our understanding of breast cancer development.

The development of technologies such as ChIP-chip, ChIP-Seq and GRO-Seq has enabled profiling of the genomic locations of NR binding in an unbiased, genome-wide manner. Studies employing these methods have revealed new insights into the mechanisms of action of nuclear receptors and highlight the complexity of nuclear receptor regulatory networks in breast cancer. In this subsection, we review new insights of NR mechanisms of action in breast cancer made possible by these genomic methods.

**Shifts from the ‘classical’ model of NR action**

Traditionally, studies on nuclear receptor action at hormone-responsive genes gave rise to the model that NRs bind proximally to the promoters of target genes, through recognition of stringent paired half-sites with highly specific orientation (Mangelsdorf et al. 1995). However, these classical models have been challenged by recent studies that profiled the genome-wide binding sites of several nuclear receptors and transcription factors using ChIP-chip or ChIP-Seq. In the context of breast cancer, genome-wide mapping of ESR1 genomic localization in the MCF-7 breast cancer cell line showed that most ESR1 binding occurs at distal regions of the genome and that many ESR1 sites did not contain the canonical ESR1-binding motif (Carroll et al. 2006). Kittler and coworkers examined the genomic distribution of the binding sites of 24 NRs in MCF-7 cells and found that NR varied significantly in their genomic localization, with both proximal-biased and distal-biased NRs being observed (Kittler et al. 2013). The observation that NRs localize not only to proximal promoter regions but also to distal regions and the prevalence of non-canonical motif and half-site recognition is also confirmed in a meta-analysis of NR cistromes in different cell types (Tang et al. 2011). NR binding at non-canonical response elements can be a mechanism to fine tune transcriptional responses of NR. For example, the glucocorticoid receptor (GR) is capable of binding a negative response element (nGRE) that confers transrepression in addition to the canonical glucocorticoid response elements (GRE) that confers transactivation to liganded GR in epidermis and intestinal epithelial cells (Surjit et al. 2011). Furthermore, NRs are capable of mediating long-range transcriptional regulation that involves chromatin looping as illustrated by studies on the estrogen receptor-mediated long-range chromatin interactions (Liu & Cheung 2014). Together, these studies suggest a more complex model of NR genomic action in which NRs frequently act on long-range enhancers whose actions can be fine-tuned by recognition of different response elements.

**Cell type specificity and the chromatin landscape**

Studies investigating NR cistromes highlight the remarkable difference in the genome-wide binding profiles of the same NR in different cell types (Krum et al. 2008, Clarke & Graham 2012). In addition to the influence of coregulators in determining the cell type-specific transcriptional response of NRs (discussed in the next section), another major aspect of NR action illuminated through advances in genomic technologies is the dynamic and complex interactions between NR and the chromatin landscape of the cell. It is becoming clear that chromatin, existing in a dynamic continuum of condensation states, regulates as well as is regulated by, NR actions, and that NR–chromatin interaction is a major determinant of NR cell type-specific transcriptional regulation. Due to the widely accepted model of NR binding to DNA only after conformational changes induced upon ligand binding, several groups have investigated the question of pre-induction vs post-induction chromatin as a determinant of NR action. Genome-wide screening of DNase I hypersensitive sites (DHS) in breast cells revealed that the majority (>70%) of GR binding occurs at pre-induction DHS sites, whereas only ~20% of GR binding occurs at hormone-induced remodeled chromatin (John et al. 2011). A recent study of long-range interactions before and after dexamethasone induction in HeLa cells found that, similar to breast cells, the majority of GR binding occurs at pre-accessible chromatin. Binding of GR to a subset of sites containing the consensus GRE results in the formation of active enhancers and increased long-range interactions (Kuznetsova et al. 2015). Profiling of ESR1 revealed a similar pattern. The majority of ESR1-binding sites coincide with pre-existing open chromatin, co-occurrence of other transcription factor binding, and correspond to cell type-specific gene regulation, whereas ESR1-binding sites shared by multiple cell types are characterized by inaccessible chromatin containing high-affinity estrogen response elements (Gertz et al. 2013). Profiling of the PGR by DNase and Micrococcal nuclease (MNase) followed by next-generation sequencing showed that PGR binding upon hormone stimulation corresponds with DHS regions that still exhibit high nucleosome occupancy. Upon hormone treatment, remodeling of nucleosomes containing functional PGR-binding sites occurs, and progesterone-responsive genes are associated with PGR-binding sites that show strong nucleosome

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remodeling upon hormone induction (Ballare et al. 2013). The chromatin landscape of the cell therefore plays an important role in determining the genomic binding profiles of specific NRs. Although some NRs such as ESR1 and GR rely mostly on pre-programmed sites made accessible by other cell- and tissue-specific pioneer DNA-binding factors, other NRs such as PGR require ligand-dependent active chromatin remodeling.

Pioneer factors and coregulators as modulators of NR function

Pioneer factors are transcription factors that can bind condensed chromatin and influence transcription by facilitating subsequent recruitment of other transcriptional regulators. Recent studies have highlighted the importance of pioneer factors in facilitating chromatin accessibility and also in determining the cell type-specific response of NRs. This is exemplified by the dependence of ESR1 on FOXA1 in breast cancer. FOXA1 expression is luminal restricted (Perou et al. 2000) and is thought to function as a pioneer factor (Cirillo et al. 2002). FOXA1 has been observed to influence genome-wide chromatin accessibility and is a key determinant of cell type-specific ESR1 genomic localization (Lupien et al. 2008, Hurtado et al. 2011), reflecting the importance of interaction with other factors on control of cell specificity of ESR1. Similarly, AP-1 has been shown to recruit GR to regions of the genome that are basally accessible prior to hormonal treatment. AP-1 is thought to maintain chromatin accessibility for GR binding as well as recruiting GR indirectly in the absence of a canonical GR motif (Biddie et al. 2011).

In addition to pioneer factors, coregulators interact with NRs and other transcription factors to facilitate transcription of target genes. According to the Nuclear Receptor Signaling Atlas (NURSA: www.nursa.org), there are 320 NR coregulators identified to date. However, this number is likely to be a gross underestimation according to a recent proteomic study (Malovannaya et al. 2011). Coregulators can assist in transcriptional regulation of NRs by facilitating chromatin accessibility, stabilizing NR–DNA interaction or facilitating indirect NR–DNA interaction through tethering (McKenna & O’Malley 2002, Millard et al. 2013).

Selective recruitment of coregulators to subsets of NR-binding sites can also be a mechanism through which transcriptional regulation of subsets of NR target genes are fine-tuned. An early study of ESR1 and steroid receptor coactivator protein (SRC) binding using promoter tiling arrays showed E2-dependent recruitment of ESR1 and SRC to E2-stimulated genes while the absence of SRC was observed at E2-repressed genes (Kininis et al. 2007). In a subsequent study, Zwart and coworkers mapped the genome-wide binding sites of several ESR1 coregulators (SRC1, SRC2, SRC3, p300 and CBP) in MCF-7 cells and showed a complex network of ESR1-coregulator binding, with preferential binding sites for each coregulator. They identified a subset of ESR1-regulated genes that are co-occupied by SRC3, but not SRC1 or SRC2, that predicts poor or good survival outcome depending on whether the genes were upregulated or downregulated (Zwart et al. 2011). Lupien and coworkers also identified association between a subset of E2-induced ESR1 binding sites co-occupied by CARM1 and gene repression, independent of the presence of FOXA1 binding. They also identified another subset of E2-induced, FOXA1-independent, ESR1 and CARM1 co-occupied sites that result primarily in repression of expression (Lupien et al. 2009). These studies demonstrate that selective interaction with different coregulators at specific subsets of target genes may be an important mechanism through which the specificity of NR action is modulated.

Due to their central role in regulating NR-mediated transcription, many coregulators are known to be involved in human diseases (Lonard et al. 2007, Lonard & O’Malley 2012). In the breast, changes in expression levels of coregulators have been implicated in the tissue-specific response to tamoxifen (Keeton & Brown 2003). The majority of coregulators show differential expression between breast cancer and normal breast tissues, as well as between ER+ and ER− breast cancers. This is accompanied by changes in the expression correlations between subsets of coregulators and specific NRs, whose expression showed prognostic value in breast cancer (Doan et al. 2014).

Coregulators are therefore critical determinants of NR-mediated transcriptional regulation in the breast and disruptions in the normal NR–coregulator interaction network are potentially an important aspect of breast cancer biology.

Combinatorial control of gene expression by NRs in breast cancer

Recent large-scale integrative analyses of transcription factor genomic localization data from the ENCODE project highlighted the extraordinary complexity of transcriptional regulation and the extensive functional crosstalk between transcription factors (ENCODE Project Consortium 2012, Gerstein et al. 2012, Xie et al. 2013). This observation also holds for NR in breast cancer.
Kittler and coworkers (Kittler et al. 2013) built a regulatory map from cistromic data of 24 NRs and 14 breast cancer-associated coregulators in MCF-7 breast cancer cells. They showed that the resulting network is highly interconnected and there are many regions in the genome coordinately occupied by multiple NRs (HOT regions). These HOT regions are enriched with features associated with active regulatory elements, including active chromatin marks and increased chromatin accessibility. These regions are also enriched with breast cancer-relevant genes and are hypothesized to be important active regulatory regions in breast cancer cells.

On a smaller scale, other studies have also revealed convergence in genomic binding between ESR1 and various other NRs in breast cancer cells by individually comparing the overlap of their cistromes. ESR1 is known to drive growth and proliferation in the majority of breast tumors. Mounting evidence indicates that ESR1 does not act on its own and that other transcription factors, including other NRs, are important determinants of ESR1 action in breast cancer cells. For example, retinoic acid has been shown to inhibit proliferation in breast cancer cells and antagonize the growth stimulation effect of estrogen (Fontana et al. 1992). Studies of ESR1 and RARA cistromes showed that ESR1 and RARA share very similar binding profiles, although whether the interaction is antagonistic or co-operative is still controversial (Hua et al. 2009, Ross-Innes et al. 2010). Likewise, cistromic profiling of ESR1 and GR in mouse mammary epithelial cell lines revealed significant co-operation of these two NRs, through an assisted loading mechanism, in which binding of one NR facilitates chromatin remodeling thereby enabling access to DNA for the other NR (Miranda et al. 2013). Another study profiling ESR1 and GR genomic localization in MCF-7 cells revealed that, although GR co-occupies several ESR1-binding sites in cells treated with both E2 and dexamethasone, GR recruitment to these sites is associated with displacement of ESR1 leading to the repression of estrogen receptor-mediated transcriptional activation of target genes (Karmakar et al. 2013). Therefore, although ESR1 co-occupies many target genes with RARA as well as GR, the nature of their interaction is reported to be both co-operative and antagonistic, perhaps reflecting different time, target and cell-specific modes of co-operation between these NRs.

In addition to RARA and GR, ESR1 was reported to share genomic binding sites with PGR and LRH-1. In the presence of both estrogen and progesterone, PGR was shown to be recruited to the ESR1 complex and to redirect ESR1-binding events, resulting in a gene expression profile associated with better clinical outcome (Mohammed et al. 2015). However, in the presence of estrogen alone, un-ligated PGRB activated a subset of ER target genes by acting as a molecular scaffold for the formation of a transcriptional complex with ESR1 and PELP1, resulting in a more aggressive proliferative response to estrogen (Daniel et al. 2015). It is likely that the action of ESR1 and PGR and their crosstalk are highly context dependent. Furthermore, the majority of data are derived from cell line models, and the implications for breast cancer in vivo are yet to be established. LRH-1 was reported to share a substantial portion (~35%) of its binding sites with that of ESR1 and synergistically regulate a subset of estrogen-responsive genes in MCF-7 cells (Lai et al. 2013).

These studies highlight the complexity of cross talk, particularly between ER and other NRs, in gene regulatory networks and the utility of integrated, genome-wide analyses in unraveling this complexity. Whether the studies so far reflect transcriptional plasticity that is particularly a feature of ER or whether data will emerge supporting this as a mechanism common to other NRs is still to be determined; nevertheless, these insights into the functional interactions between NRs in breast cancer have the potential to lead to novel therapeutic strategies.

Reprogramming of NR binding and disease progression

It is becoming increasingly evident that transcriptional regulation is a highly dynamic process with transcription factors displaying temporal, cell type specific and disease-associated shifts in their genomic binding profiles. The transcriptional targets of PGR in T-47D breast cancer cells and AB-32 immortalized normal breast cells display remarkably low overlap (Clarke & Graham 2012), reflecting cancer-associated and cell type-specific changes in PGR transcriptional regulation. Recent studies have highlighted the effect of changes in NR transcriptional programs and their association with breast cancer disease progression and clinical outcomes. Ross-Innes and coworkers performed ChIP-seq of ESR1 in clinical samples with different prognoses to directly explore the correlation between ESR1 binding and cancer progression (Ross-Innes et al. 2012). They observed high signal intensity at ESR1-binding sites in metastatic samples, whereas lower ESR1 signal intensity was observed in samples with good prognosis. Further, they showed that ESR1 binding is a highly dynamic process, with distinct ESR1-binding regions observed in samples with different outcomes. This dynamic change in ESR1 action was shown to be influenced by...
the action of other NRs, such as PGR (Mohammed et al. 2015), as well as the signaling context leading to ESR1 activation. For example, ESR1 displayed distinct genomic binding profiles depending on whether ESR1 was activated by estrogen or through the epidermal growth factor (EGF) pathway (Lupien et al. 2010). The EGF-induced ESR1 cistrome specifically regulates genes that are overexpressed in ERBB2-positive breast cancers and associated with poor clinical outcomes. The EGF pathway can therefore be an alternative activator for ESR1 signaling in breast cancer and provides a molecular explanation for the endocrine therapy resistance often seen in ER+ERBB2+ breast cancers. Analysis of ESR1 and ESRRB cistromes in tamoxifen-sensitive vs -resistant breast cancer cells showed that despite regulating distinct transcriptional networks, their cistromes are reprogrammed in tamoxifen-resistant breast cancer cells toward the regulation of genes functionally relevant to resistance (Thewes et al. 2015). These studies show that NR binding profiles can be shifted in a context-dependent manner, resulting in altered transcriptional networks that affect disease progression and outcome.

### Emerging functional roles of NR in BC

It is now clear that a number of NRs are implicated in breast cancer growth and development (Conzen 2008). It is emerging that, in addition to influencing cell growth and proliferation, NRs also play important roles in other aspects of breast cancer biology. Table 2 summarizes reported involvement of NRs in selected aspects of breast cancer biology. This section outlines some of the emerging functional roles of NRs in breast cancer.

### Nuclear receptors as key components of the circadian clock

A circadian rhythm is any biological process that displays an endogenous, entrainable oscillation cycle of roughly 24 h, driven by a self-sustained timekeeping mechanism, the circadian clock. The circadian clock governs many aspects of human physiology, including body temperature, sleep–wake cycle, blood pressure, hormone secretion and metabolism. In line with this, at least 10% of all genes are under the control of the circadian system and display

### Table 2 NR function in breast cancer

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Symbol</th>
<th>Anti-proliferative</th>
<th>Pro-apoptotic</th>
<th>Anti-migratory</th>
<th>Pro-oxidative phosphorylation</th>
<th>Pro-proliferative</th>
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*NR effect on cancer-related biological processes based on studies in breast primary tissue or cell lines. The influence of NR on breast cancer proliferation, apoptosis, migration, metabolism as well as involvement in circadian regulation/response is tabulated. Y, indicates reported involvement.
circadian oscillation (Akhtar et al. 2002, Oishi et al. 2003, 2005). There is mounting evidence linking circadian disruption to various clinical and pathological conditions including cancer. Here, we discuss the emerging link between NRs and circadian regulation, as well as the growing body of evidence linking circadian disruption and breast cancer.

Initially, the circadian clock was defined to be a relatively simple feedback loop consisting of the key transcription factors CLOCK and BMAL and their co-repressors, PER and CRY (Fig. 2). It is now emerging that the circadian clock contains other auxiliary loops that involve multiple NRs, most prominently REV-ERBs and RORs (Fig. 2, reused from Bechtold et al. (2010), with permission from Elsevier). RORs recognize the same regulatory elements as REV-ERBs, and a range of studies have demonstrated their importance in the regulation of clock gene expression (Akashi & Takumi 2005). Gene deletion studies and cistrome analyses have confirmed the pivotal role of REV-ERBs in the universal circadian machinery (Preitner et al. 2002).

In addition to REV-ERBs and RORs, several other NRs have been shown to regulate as well as being regulated by the circadian clock, most notably GR (Conway-Campbell et al. 2010) and ESRRA (Dufour et al. 2011). The list of other NRs potentially under control of the circadian clock is extensive, with at least 35 NRs known to display circadian expression in various metabolic tissues (Zhao et al. 2014).

Figure 2
The molecular clock machinery (reprinted from Trends in Pharmacological Sciences, volume 31, Bechtold DA, Gibbs JE & Loudon AS, Circadian dysfunction in disease, pages 191–198, copyright (2010), with permission from Elsevier). The molecular machinery that provides circadian timekeeping consists of a complex circuitry of transcriptional/translational regulatory feedback loops (clock components shown in gray). In mammals, the current model involves a primary loop with CLOCK (or homologue NPAS2) and BMAL1 as transcriptional activators, and PERIOD (PER1, PER2 and PER3) and CRYPTOCHROME proteins (CRY1 and CRY2) as transcriptional repressors. As levels of cytosolic PER and CRY proteins rise, they associate, translocate to the nucleus and repress their own gene transcription through direct interaction with the CLOCK/BMAL1 complex. This feedback cycle provides near 24-h timing and drives the rhythmic expression of several clock-controlled and clock-modulated genes, which in turn mediate circadian rhythms in behavior and physiology. Acting on the primary feedback loop are auxiliary loops, which appear to increase the stability and robustness of the oscillations. The most notable interlocking loop is that involving the nuclear hormone receptors (NRs), REV-ERB and ROR. In addition to REV-ERB and ROR, several other NRs (shown in green) interact closely with the circadian feedback loops and are responsive to the clock (exhibit rhythmic expression) and able to feedback onto the clock genes themselves. NR regulation of clock genes also renders the clock responsive to numerous circulating hormones (e.g. cortosol, estrogen), nutrient signals (e.g. derivatives of fatty acids and retinoids) and cellular redox status (NADH/NAD+ ratio).
To date, epidemiological studies reported mixed findings on the association between increased risk of breast cancer and circadian disruption in the form of night shift work. Although a few studies reported no significant association between breast cancer and night work (O’Leary et al. 2006, Pronk et al. 2010), the majority of recent studies reported significant or borderline associations, with the strongest association found with long-term exposure to night work (Hansen et al. 2001, Schernhammer et al. 2001, 2006, Hansen & Lassen 2012, Hansen & Stevens 2012, Knutsson et al. 2013, Menegaux et al. 2013, Rabstein et al. 2013, Akerstedt et al. 2015, Papantoniou et al. 2015). Meta-analysis studies have also reported a positive association between night work and breast cancer risk (Jia et al. 2013) and that a positive dose–response gradient is observed for breast cancer with increased years of night shift and cumulative night work (Wang et al. 2013).

Although circadian disruption is prominently linked to breast cancer tumorigenesis through epidemiological studies, the molecular mechanisms and NRs involved are still largely unknown, with most published studies focusing on the ESR1 as a link between the circadian system and breast cancer development. Many studies suggest that lowered melatonin level due to exposure to night light contributes toward breast cancer development and drug resistance. Melatonin is thought to exert its oncostatic effect through multiple mechanisms including anti-mitosis, anti-angiogenesis, anti-oxidation and regulation of immune response (Viswanathan & Schernhammer 2009). The oncostatic effect of melatonin in breast cancer is thought be mediated through its anti-estrogenic actions as well as its role in regulating the activity of aromatas, the enzymes responsible for the local biosynthesis of estrogens from androgens (Cos et al. 2006). Recent studies using MCF-7 breast cancer xenografts in mice showed that suppression of melatonin production by dim light exposure at night leads to both tamoxifen (Dauchy et al. 2014) and doxorubicin resistance (Xiang et al. 2015).

In addition to the effect of melatonin, there is evidence linking the core clock genes as well as the REV-ERBs with breast cancer growth and metastasis. The rhythmic expression of the PER genes are reported to be altered in primary breast tumors (Chen et al. 2005) as well as in breast cancer cell lines (Xiang et al. 2012). A recent study demonstrated the association of the core clock gene BMAL2 in ER breast cancer metastasis (Ha et al. 2016). Furthermore, activation of REV-ERBA and REV-ERBB by a synthetic ligand is anti-proliferative in breast cancer cells.

ESR1 has been shown to be an important regulator linking the circadian system and breast cancer tumorigenesis, acting as a regulator of (as well as being regulated by) the core clock genes. ESR1 appears to participate in a feedback loop involving the clock protein PER2, which was shown to be a tumor suppressor in luminal breast cancer. Although PER2 is E2 inducible, PER2 itself is thought to mediate ESR1 degradation through the proteasome pathway. Suppression of PER2 leads to ESR1 stabilization (Gery et al. 2007). In addition, ESR1 was shown to bind estrogen response elements in the promoter region of CLOCK leading to the upregulation of CLOCK in breast cancer cells. Knockdown of CLOCK attenuated proliferation in breast cancer cells (Xiao et al. 2014). Therefore, CLOCK appears to be an important mediator of the proliferative effect of E2 in breast cancer.

In summary, NRs play important regulatory roles in both the universal and tissue-specific circadian systems. In particular, REV-ERBs and RORs are integral regulators of the universal circadian clock, and various other NRs exhibit circadian expression. Although epidemiological studies have linked circadian disruption and breast cancer tumorigenesis, a lot remains to be learned about the underlying molecular mechanism. Lowered melatonin due to night light exposure is thought to play a role and there is evidence supporting the involvement of ESR1 as an integral regulator linking circadian regulation and breast cancer development.

Regulation of energy metabolism

As the initial observation by Warburg that proliferating tumor cells converted the majority of their glucose to lactate even in oxygen-rich condition and his hypothesis that altered metabolism is a characteristic of cancer cells, metabolic reprogramming has now attained cancer hallmark status (Ward & Thompson 2012). Specifically, the Warburg effect describes a shift toward aerobic glycolysis in preference to oxidative phosphorylation as the major means of ATP generation in cancer cells, even in oxygen-rich conditions. Although aerobic glycolysis is not as efficient as oxidative phosphorylation (yielding only 2 mol of ATP/mole of glucose instead of 36 mol ATP/mole of glucose), it has certain benefits for tumor cells. Glycolysis results in more rapid production of ATP, fatty acids and nucleotides that are needed by proliferating tumor cells that need to double their biomass to divide. Furthermore, the generation of lactic acid promotes a tumor microenvironment that is protective against
immune attack (Calcino et al. 2012). It has also been suggested through glucose flux modeling that accumulation of glucose actually promotes aerobic glycosis in preference to oxidative phosphorylation (Vazquez et al. 2010); hence, glucose flux can potentially act as a trigger for the Warburg effect.

It has emerged that NRs are centrally placed in many of the pathways controlling energy metabolism, from regulating glucose transporters to controlling the downstream pathways involved in glucose metabolism. Their altered expression in breast cancers is potentially intimately linked to the metabolic reprogramming of the tumors cells. Here, we review our current understanding of the roles of NRs in breast cancer cellular metabolism.

REV-ERBs In addition and related to their prominent roles in circadian regulation, REV-ERBs are recognized as integrators of circadian regulation and metabolic pathways (Cho et al. 2012, Gerhart-Hines & Lazar 2015). A recent study looking at genome-wide location of REV-ERBA in various tissues reported different mechanisms of gene regulation employed by REV-ERBA with regard to circadian control and metabolic control. Although circadian regulation requires direct DNA binding of REV-ERBA to its cognate site, metabolic control involves the recruitment of HDAC3, which is tethered by cell type-specific transcription factors (Zhang et al. 2015). A recent publication suggests that although REV-ERBA has a dominant role in normal cells, REV-ERBB seems to be the dominant isoform controlling both circadian rhythm and metabolic pathways in cancer cells, including breast cancer (De Mei et al. 2015). REV-ERBB is significantly more abundant in cancer cells compared to REV-ERBA, whereas the opposite is observed in normal cells. Knockdown of REV-ERBB resulted in the enhanced expression of both circadian and metabolic target genes in breast cancer cells while knockdown of REV-ERBA had no effect. However, ERBB2-positive breast cancer cells appear to have higher expression of REV-ERBA compared to ERBB2-negative cells, consistent with a previous study reporting co-expression of REV-ERBA and ERBB2 and pro-survival function of REV-ERBA in ERBB2-positive breast cancer cells (Kourtidis et al. 2010). These studies suggest that the two REV-ERB isoforms probably have redundant functions in transcriptional regulation, and functional predominance in a particular cell type depends on the relative expression level of each isoform.

Estrogen-related receptors (ERRs) The estrogen-related receptors (ESRRA/NR3B1, ESRRB/NR3B2 and ESRRG/NR3B3) have become recognized as the master regulators of energy metabolism in multiple tissues with high energy demand (Giguere 2008, Deblois & Giguere 2013). Both ESRRA and ESRRG have dominant roles in maintaining energy homeostasis through the regulation of metabolic gene networks. In the heart, ESRRA and ESRRG co-operate to control genes involved in uptake of energy substrates, production and transport of ATP across the mitochondrial membrane (Alaynick et al. 2007, Dufour et al. 2007). ESRRG was reported to co-operate with the peroxisome proliferator-activated receptor-gamma coactivator alpha gene (PGC-1α) in a double-positive feedback loop to regulate the expression of many oxidative phosphorylation genes in mouse myoblast cells (Mootha et al. 2004). In the liver, ESRRG was reported to co-operate with PROX1 and BMAL1 to regulate circadian and metabolic gene networks (Dufour et al. 2011). Together, the three ERR isoforms recognize the proximal regulatory regions of 705 genes involved in all aspects of mitochondrial biogenesis and function (Eichner & Giguere 2011).

In the breast, ESRRA and ESRRG are associated with distinct survival outcomes (Ariazi et al. 2002). Although ESRRA is associated with increased recurrence and poor outcome (Thewes et al. 2015), ESRRG expression is correlated with ESR1 and ERBB4, which are markers of favorable outcome (Ariazi et al. 2002). It has been suggested that ESRRA and ESRRG have opposite roles in the regulation of metabolic reprogramming of breast cancer cells (Deblois & Giguere 2013). Although ESRRG promotes aerobic glycolysis through the upregulation of enzymes that regulate the glycolysis pathway (Cai et al. 2013), ESRRG is thought to sustain oxidative phosphorylation through regulation of genes that control the tricarboxylic acid cycle (Eichner et al. 2010). However, metabolic reprogramming by ERRs in breast cancers probably involves much greater complexity, given that overexpression of ESRRG also leads to increased expression of enzymes in the glycolytic pathways (Cai et al. 2013) and that ESRRA and ESRRG readily form heterodimers and bind to regulatory regions of many shared target genes (Dufour et al. 2007).

ESRRs also interact with oncogenes that are known modulators of metabolic pathways such as MYC, HIF and ERBB2. Many genes in the glycolytic pathways are regulated by MYC. ESRRA was found to participate in a complex with MYC to co-regulate glycolytic genes (Cai et al. 2013). HIF directly activates glucose transporters and the majority of genes in the glycolytic pathways. All three ESRR isoforms were identified as coactivating..
factors of HIF and to enhance HIF-induced glycolytic and angiogenic gene expression in hypoxic condition (Ao et al. 2008). ESRRA also regulates the expression of ERRβ2 (Deblois et al. 2010), which was reported to translocate to the mitochondria of tumor cells and regulate energy metabolism. Overexpression of mitochondrial ERRβ2 decreases mitochondrial electron transport chain activity and enhances cellular glycolysis (Ding et al. 2012). In addition, ERBB2 influences the glycolytic phenotype through upregulation of lactate dehydrogenase (Zhao et al. 2009) as well as REV-ERβA, an NR that was reported to be involved in glycolysis and fatty acid synthesis in breast cancer cells (Kourtidis et al. 2010).

In summary, the ERs are prominent regulators of gene networks controlling glycolysis and oxidative phosphorylation in metabolic tissues. In the breast, ESRRα expression is associated with poor outcome and appears to be involved in reprogramming the cell to favor aerobic glycolysis, a metabolic state characteristic of cancer cells. ESRRG, on the other hand, is associated with better outcome and is involved in maintaining oxidative phosphorylation, a metabolic state characteristic of normal cells. However, given that ESRRα and ESRRG can form heterodimers and readily bind to many shared target genes, the complexity of the mechanisms for controlling their specificity of action is still to be deciphered.

**Peroxisome proliferator-activated receptors** (PPARs) PPARs function as heterodimers with the retinoid receptors (RXR) and regulate various genes that are involved in lipid metabolism and energy homeostasis. Through these pathways, PPARs influence various cancer-related cellular processes such as proliferation, differentiation and survival (Michalik et al. 2004). Three PPAR isotypes (PPARα/NR1C1, PPARδ/NR1C2 and PPARγ/NR1C3) are known, each with unique expression profile and functional roles. The PPARs showed decreased expression in breast cancer compared to normal breast (Muscat et al. 2013). The role of PPARδ in breast cancer tumorigenesis is unclear. Although activation of PPARδ has been shown to inhibit breast cancer cell line tumorigenicity (Yao et al. 2014), inhibition of PPARδ by inverse agonists was reported to inhibit breast cancer cell invasione (Adhikary et al. 2013). PPARγ is the best studied of the 3 PPAR subtypes and has been reported to have an anti-proliferative effect on breast cancer cells (Pon et al. 2015) and is associated with better outcomes based on survival analysis of PPARγ protein expression level in BC tissue microarrays (Abduljabbar et al. 2015a). The downstream effect of PPAR seems to be dependent on the cell compartment in which PPARγ is activated though, with activation in cancer cells resulting in growth inhibition while activation in stromal cells results in growth enhancement of co-injected breast cancer cells (Avena et al. 2013). Recent studies have also suggested an involvement of PPARγ and energy metabolism in breast cancer. Firstly, several genes controlling the glycolytic pathways are found to have peroxisome proliferator response element (PPRE) suggesting their regulation by PPARs (Sakharkar et al. 2013). Secondly, overexpression of PPARγ in fibroblasts increased the production of l-lactate and mitochondrial dysfunction. In addition, PPARγ induces the activation of HIF1α, a transcription factor that promotes glycolysis (Avena et al. 2013).

**Control of breast cancer migration and metastasis**

Breast cancer metastasis accounts for the majority of deaths from breast cancer. Early detection and a deeper understanding of the metastatic process are critical to develop therapeutic interventions. Metastasis involves a complex cascade of steps starting with invasion by the primary tumor of the surrounding host tissues, followed by intravasation and dissemination of the tumors cells via the blood or lymphatic system, infiltration and colonization at the distant site. Several factors and pathways are known to influence cancer metastasis including disintegration of cell-to-cell adhesion, proteolytic remodeling of the extracellular matrix, cell motility, evasion of immune and apoptotic signals and angiogenesis. Although substantial information is known about the process of metastasis, the molecular basis of breast cancer metastasis remains poorly understood. NRs, being master regulators of almost every physiological aspect of life, are likely to be intimately involved in the metastasis process. Here, we summarize the current understanding of the roles of various NRs in biological pathways affecting breast cancer metastasis.

**Estrogen receptors** The estrogen receptors alpha (ESR1) and beta (ESR2) appear to have distinct roles in breast cancer progression and metastasis, with reports of ESR1 signaling enhancing breast cancer cell migration and invasion, whereas ESR2 signaling has the opposite effects.

Emerging evidence suggests that estradiol’s positive effect on cell migration and invasion appears to be mediated through ESR1’s extranuclear signaling. ESR1 extranuclear signaling is mediated through the PI3K, MAPK and c-Jun N-terminal kinase pathways (Li et al. 2010, Zheng et al. 2011) with the involvement of PELP1 (Chakravarty et al. 2010), focal adhesion kinase (FAK)
(Sanchez et al. 2010), C-Src and paxillin (Li et al. 2010) for activation. Downstream activation of the RhoA/ROCK-2 cascade has also been reported (Giretti et al. 2008, Zheng et al. 2011). Recruitment of the actin-binding protein moesin (Giretti et al. 2008) and phosphorylation of the actin-binding protein ezrin (Zheng et al. 2011) were reported as possible mechanisms through which ESR1 signaling influences the cytoskeletal organization. These E2-mediated signaling pathways induce features of motile cells such as dynamic actin cytoskeleton remodeling and formation of ruffles and filopodia-like structures, which resulted in enhanced motility and migration of breast cancer cells (Chakravarty et al. 2010).

ESR2, on the other hand, has been associated with less invasive and proliferative tumors (Jarvinen et al. 2000, Lazennec et al. 2001). Overexpression of ESR2 leads to reduced cell growth and mobility (Li et al. 2012) and ESR2 was reported to upregulate E-cadherin (Zhou et al. 2015), integrin alpha1, integrin beta1 and enhance the formation of vinculin-containing focal complexes and actin filaments (Lindberg et al. 2010), which consequently strengthens cell adhesion and reduces migration and invasion.

However, ESR2’s influence on cell migration is possibly more complex than simply having an anti-migratory and anti-proliferative effect, with contradictory reports of ESR2 having both pro-invasive and pro-migratory effects, especially in specific breast cancer subtypes, due to crosstalk with ESR1 as well as differential effect of different ESR2 variants. ESR2 and PEA3 were reported to co-activate IL-8 resulting in increased invasiveness in ER+ MCF-7 cells (Chen et al. 2011). In inflammatory breast cancer cells, which express both ESR2 and ESR1β (an ESR1 variant), it was suggested that non-genomic signaling involving ESR1β, ESR2 and GRPR30 through activation of p-ERK1/2 to have pro-migratory and pro-invasive effect (Ohshiro et al. 2012). Furthermore, expression of an ESR2 variant, ESR2cx in primary tumors, was reported to correlate with higher risk of lymph node metastasis (Rosin et al. 2014). In summary, the effects of estrogen receptor signaling on breast cancer cell metastasis is complex with different isoforms having opposing roles, which is further complicated by divergent effects of subtype variants and crosstalk. The emerging picture is that of ESR1 exerting pro-migratory and pro-invasive effects through extranuclear signaling to regulate cell adhesion and cytoskeletal remodeling while ESR2 exerts the opposite effect through as yet unclear mechanisms.

**Progestosterone receptors** PGR in the human is expressed as two functionally different forms (PGRA and PGRB) arising from alternate promoter activities driving a single gene (Kastner et al. 1990). PGRA and PGRB are equivalently expressed in most normal cells, but commonly their expression becomes deregulated in breast cancer resulting in a predominance of one isoform (usually PGRA) (Graham et al. 1995). This disruption is seen early in disease progression (Mote et al. 2002) and is associated with a poorer response to the anti-estrogen tamoxifen (Mote et al. 2015). A number of studies have demonstrated progestin effects on breast cancer cell adhesion, migration and invasive potential. However, these effects are ligand, PGR isoform and context dependent. In general, progestins acting through nuclear PGR inhibit cell migration and invasiveness (Lin et al. 2000, 2001, McGowan et al. 2004, Carnevale et al. 2007). In cells transfected with PGR, progestin treatment increases actin stress fibers and focal contacts, consistent with increased adhesion and decreased migration (Lin et al. 2000, 2001). Invasion of T-47D breast cancer cells, expressing equivalent PGR isoform levels, is inhibited by progestins (McGowan et al. 2004). However, predominance of PGRA results in an altered progestin response, including increased focal adhesion signaling (Graham et al. 2005), enhanced migration and increased invasion (McGowan et al. 2004), potentially contributing to the poorer outcomes seen in PGRA-predominant breast cancers.

Crosstalk between PGR and cytoplasmic signaling pathways is implicated in breast cancer migration and metastasis. Using a DNA-binding mutant PGR, Carnevale and coworkers (Carnevale et al. 2007) reported that PGR activated cytoplasmic signaling cascades that contributed to breast cancer metastasis. Progestin activation of MAPK, PI3K/Akt and GTPase/RhoA modulated the expression of genes such as urokinase plasminogen activator (uPA), uPA receptor (uPAR), matrix metalloproteinases (MMPs), β1-integrin and PAI-1 (Carnevale et al. 2007, Fu et al. 2008, Bellance et al. 2013) suggesting a mechanism through which migration is increased by progestins. In addition, progestone/progestins also enhance the phosphorylation of focal adhesion kinase (FAK) (Graham et al. 2005, Fu et al. 2008, Bellance et al. 2013), and this is enhanced with PGRA predominance (Graham et al. 2005), promoting the formation and turnover of focal adhesion points and cytoskeletal reorganization involved in cellular motility and influencing breast cancer progression and metastasis (Luo & Guan 2010).
PGR has also been reported to exert ligand-independent effects on breast cancer cell morphology and migration (Jacobsen et al. 2005, Carnevale et al. 2007, Bellance et al. 2013). Un-ligated PGRA was shown to differentially regulate genes involved in cell adhesion and increase adhesiveness and migration in inducible cells expressing just one isoform (Jacobsen et al. 2005). However, in a recent study using bi-inducible MDA-MB-231 cells, un-ligated PGRB but not PGRA increased cell migration via differential effects on focal adhesion signaling (Bellance et al. 2013). Furthermore, it has been demonstrated that extensive ligand-independent action of PGRB are dependent on specific post-translational modifications, particularly phosphorylation, and associated with pro-survival pathways (Daniel et al. 2007, Faivre et al. 2008, Knutson et al. 2012). These findings in the absence of ligand suggest that disrupted PGR isoform expression may have particular importance in the context of post-menopausal breast cancer, where circulating progesterone is low or absent.

In summary, the emerging picture is that the effects of PGR and progesterone on breast cancer metastasis, adhesion and invasion are context dependent and influenced by the relative ratio of PGR isoforms being expressed, the presence of ligands and whether PGR functions as a transcription factor or activator of signaling cascades, but that PGR contributes to increased invasive and metastatic behavior in a number of contexts.

**Retinoic acid receptors** Several studies demonstrated the anti-proliferative and anti-migratory effect of retinoids on breast cancer cells. Specifically, all-trans retinoid acid (ATRA) was reported to modulate several migration-related proteins such as downregulation of MMP-1, MMP-2, MMP-9, FAK, NF-κB and p-ERK and upregulation of E-cadherin in breast cancer cell lines (Liu et al. 2003, Dutta et al. 2009, 2010). The anti-migratory effect of retinoids on breast cancer cells were shown to be mediated through RARB with treatment of RA or RARB agonist resulting in significantly reduced cell migration while treatment with RARA or RARG agonists did not (Flamini et al. 2014). RARB is the only member of the RARs showing decreased expression in breast cancers (Muscat et al. 2013). RARB showed progressively decreased expression during breast carcinogenesis, with only around 50% of invasive breast carcinoma expressing RARB (Xu et al. 1997). Transduction of RARB2 resulted in significant reduction in metastasis rate in a mouse xenograft model (Treutling et al. 2002). Together, these findings highlight that RARB is necessary for mediating the anti-migratory effect of retinoic acid through modulation of expression of genes involved in cell migration.

**Estrogen-related receptors** Aside from their prominent role as master regulators of energy metabolism, the ERRs have been reported to influence the migratory potential of breast cancer cells. Knockdown of ESRRB dramatically decreased the migratory potential of breast cancer cells (Stein et al. 2008), later determined to be mediated through VEGF (Stein et al. 2009) and WNT11 (Dwyer et al. 2010) signaling pathways, which are known regulators of angiogenesis. Inactivation of ESRRB also resulted in impaired directional migration of breast cancer cells, mediated through enhanced stability of RHOA, a protein involved in controlling oriented cellular migration (Sailland et al. 2014). ESRRB itself was found to be a target of miR-137 (Zhao et al. 2012). Therefore, consistent with reports of its association with poor prognosis, activation of ESRRB has a pro-migratory effect on breast cancer cells. By contrast, and consistent with its association with better breast cancer outcome, ESRRG was reported to promote mesenchymal-to-epithelial transition and decrease breast cancer cell invasiveness through activation of E-cadherin (Tiraby et al. 2011). Therefore, similar to their opposing roles in metabolic reprogramming, ESSRA and ESSRG display opposing influences on breast cancer cell migration and invasiveness.

**NUR77** NUR77 (NR4A1) expression is elevated in both ER+ and ER– breast tumors (Muscat et al. 2013), and NUR77 expression is correlated with decreased relapse-free survival in breast cancer (Alexopoulou et al. 2010), consistent with reports of its pro-oncogenic role in breast cancer (Hedrick et al. 2015). Contradictory to a previous report of NUR77 having anti-migratory effects in MCF-10A breast cancer cells, recently, NUR77 expression was shown to have pro-migratory effects through activation of TGF-beta signaling (Zhou et al. 2014), which is known to have an important role in breast cancer metastasis (Moore et al. 2008, Kohn et al. 2012, Luwor et al. 2015).

**COUP-TF1 and COUP-TF2** COUP-TFs are orphan nuclear receptors primarily known for their important roles in organogenesis including angiogenesis, cellular growth, differentiation and migration (Boudot et al. 2011). Their roles in breast cancer growth and progression have recently been highlighted. Both COUP-TF1 and COUP-TF2 expression are lower in breast tumors.
compared to normal breast tissue (Muscat et al. 2013). COUP-TF1 expression was reported to be higher in dedifferentiated breast cancer cells and correlated with low expression of E-cadherin and expression of vimentin (Le Dily et al. 2008). Overexpression of COUP-TF1 in MCF-7 cells results in a decrease in CXCL12 and increase in CXCR4 expression, mediated by EGF signaling, and leads to enhanced motility and invasiveness of MCF-7 breast cancer cells (Le Dily et al. 2008, Boudot et al. 2014). CXCL12 expression in primary tumors has recently been reported to drive breast cancer metastasis (Ray et al. 2015). The other COUP-TF member, COUP-TF2, may also have a role in breast cancer cell migration and invasion with a report that transfection of COUP-TF2 into MDA-MB-231 resulted in increased migration and invasion of these cells (Navab et al. 2004). Together these findings suggest a potential involvement of COUP-TFs in epithelial-to-mesenchymal transition and migration of breast cancer cells.

Concluding remarks

Advances in genomic technologies have enabled more integrated insights into the roles of NRs in breast cancer biology: their expression, genomic distribution, mechanisms of action, as well as the complexity of their functional interactions. Expression profiling studies have shown that many NRs, in addition to ESR1 and PGR, are expressed and are potentially functional in breast cancer. Cistromic profiling studies highlight the complexity of NR transcriptional regulation, how multiple NRs often work together as well as with other coregulators and the chromatin landscape to fine tune the cell-specific expression of target genes, and how changes in the gene regulatory programs of NR are associated with the tumor state. Finally, it is evident that in addition to regulating proliferation and apoptosis, NRs are critical regulators of a diverse range of other cancer-associated biological processes including the circadian clock, metabolic reprogramming and migration and metastasis.

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